

OIPE

RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/961,376

TIME: 11:47:00

Input Set : A:\PF524P1 SEQ LIST 09 25 2001.txt

Output Set: N:\CRF3\10092001\I961376.raw

3 <110> APPLICANT: Ruben et al.
5 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
7 <130> FILE REFERENCE: PF524P1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/961,376
10 <141> CURRENT FILING DATE: 2001-09-25
12 <150> PRIOR APPLICATION NUMBER: 60/254,874
13 <151> PRIOR FILING DATE: 2000-12-13
15 <150> PRIOR APPLICATION NUMBER: 60/235,991
16 <151> PRIOR FILING DATE: 2000-09-26
18 <150> PRIOR APPLICATION NUMBER: 09/533,822
19 <151> PRIOR FILING DATE: 2000-03-24
21 <150> PRIOR APPLICATION NUMBER: 60/188,208
22 <151> PRIOR FILING DATE: 2000-03-10
24 <160> NUMBER OF SEQ ID NOS: 7
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 882
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(882)
37 <400> SEQUENCE: 1
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40 1 5 10 15
42 cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg gtg gct atg aga 96
43 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
44 20 25 30
46 tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg ggt acc tgc atg 144
47 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
48 35 40 45
50 tcc tgc aaa acc att tgc aac cat cag agc cag cgc acc tgt gca gcc 192
51 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
52 50 55 60
54 ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc aag ttc tat gac 240
55 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
56 65 70 75 80
58 cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga cag cac 288
59 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
60 85 90 95
62 cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg 336
63 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
64 100 105 110
66 aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt gaa aac 384
67 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
68 115 120 125

#2.

ENTERED

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70 aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga ggc tca 432
71 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
72      130      135      140
74 gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg 480
75 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
76 145      150      155      160
78 gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc 528
79 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
80      165      170      175
82 tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc 576
83 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
84      180      185      190
86 tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct 624
87 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
88      195      200      205
90 tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc 672
91 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
92      210      215      220
94 gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg gcg ccc 720
95 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
96 225      230      235      240
98 acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct 768
99 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
100      245      250      255
102 gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca 816
103 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
104      260      265      270
106 cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag 864
107 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
108      275      280      285
110 ggg ggc cca ggt gca taa 882
111 Gly Gly Pro Gly Ala
112      290
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116 <211> LENGTH: 293
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
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122      1      5      10      15
123 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
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125 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
126      35      40      45
127 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
128      50      55      60
129 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
130      65      70      75      80
131 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His

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132          85          90          95
133 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
134          100          105          110
135 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
136          115          120          125
137 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
138          130          135          140
139 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
140 145          150          155          160
141 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
142          165          170          175
143 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
144          180          185          190
145 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
146          195          200          205
147 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
148          210          215          220
149 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
150 225          230          235          240
151 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
152          245          250          255
153 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
154          260          265          270
155 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
156          275          280          285
157 Gly Gly Pro Gly Ala
158          290
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163 <211> LENGTH: 733
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 3
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169 aattcgaggg tgcaccgtca gtcttctctt tcccccaaaa acccaaggac accctcatga 120
170 tctcccgga ccttgaggtc acatgcgtgg tggaggacgt aagccacgaa gaccctgagg 180
171 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
172 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
173 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
174 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
175 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
176 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
177 ccacgcctcc cgtgctggac tccgacggt ccttcttctt ctacagcaag ctcaccgtgg 600
178 acaagagcag gtggcagcag gggaacgtct tctcatgtct cgtgatgcat gaggtcttgc 660
179 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
180 gactctagag gat 733
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 9
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens

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188 <220> FEATURE:
189 <221> NAME/KEY: SITE
190 <222> LOCATION: (1)..(5)
191 <223> OTHER INFORMATION: Xaa equal any amino acid
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194 <221> NAME/KEY: SITE
195 <222> LOCATION: (9)
196 <223> OTHER INFORMATION: Xaa equal any amino acid
198 <400> SEQUENCE: 4
W--> 199 Xaa Xaa Xaa Xaa Xaa Glu Gly Ser Xaa
      200   1           5
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 9
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <221> NAME/KEY: SITE
210 <222> LOCATION: (3)
211 <223> OTHER INFORMATION: Xaa equal is any amino acid
213 <400> SEQUENCE: 5
W--> 214 Ala Leu Xaa Asn Asp Glu Gly Ser Gly
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217 <210> SEQ ID NO: 6
218 <211> LENGTH: 17
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo Sapiens
222 <400> SEQUENCE: 6
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227 Ala
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231 <211> LENGTH: 22
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: SIGNAL
237 <222> LOCATION: (1)..(22)
238 <223> OTHER INFORMATION: consensus signal sequence
240 <400> SEQUENCE: 7
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      243   1           5           10           15
245 Trp Ala Pro Ala Arg Gly
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VERIFICATION SUMMARY

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Input Set : A:\PF524P1 SEQ LIST 09 25 2001.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5